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                    GenCore version 4.5
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OM protein - protein search, using sw model

Run on:          March 14, 2002, 17:24:09 ; Search time 37.43 Seconds
                                          (without alignments)
                                          29.387 Million cell updates/sec

Title:           US-09-786-009-6
Perfect score:   166
Sequence:        1 CAYKITQANKHIIVACEGNPYVPVHFDASV 30

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters:      100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SwissProt_39:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                 %
Result          Query
  No.   Score   Match Length DB  ID                         Description
----------------------------------------------------------------------------
     1    166   100.0    150  1  RNP_BOVIN                  P00656 bos taurus
     2    163    98.2    124  1  RNP_BUBBU                  P00657 bubalus bub
     3    160    96.4    124  1  RNP_AEPME                  P07847 aepyceros m
     4    160    96.4    124  1  RNP_GAZTH                  P07818 gazella tho
     5    160    96.4    124  1  RNP_SHEEP                  P00661 ovis aries
     6    157    94.6    124  1  RNP_ANTAM                  P00668 antilocapra
     7    156    94.0    124  1  RNP_ALCAA                  P00667 alces alces
     8    156    94.0    124  1  RNP_CAPCA                  P00664 capreolus c
     9    156    94.0    124  1  RNP_RANTA                  P00666 rangifer ta
    10    155    93.4    124  1  RNP_CONTA                  P00660 connochaete
    11    154    92.8    124  1  RNP_DAMKO                  P00659 damaliscus
    12    153    92.2    124  1  RNP_GIRCA                  P00662 giraffa cam
    13    152    91.6    124  1  RNP_TRAST                  P00658 tragelaphus
    14    151    91.0    124  1  RNP_CEREL                  P00663 cervus elap
    15    151    91.0    124  1  RNP_DAMDA                  P00665 dama dama (
    16    147    88.6    124  1  RNP_AXIPR                  P87351 axis porcin
    17    146    88.0    124  1  RNP_BOSTR                  P07849 boselaphus
    18    145    87.3    124  1  RNP_BALAC                  P00673 balaenopter
    19    145    87.3    149  1  RNP_MOUSE                  P00683 mus musculu
    20    144    86.7    128  1  RNP_HORSE                  P00674 equus cabal
    21    143    86.1    124  1  RNP_HIPAM                  P00672 hippopotamu
    22    141    84.9    149  1  RNP_URARU                  Q9wux6 uranomys ru
    23    140    84.3    124  1  RNP_CAMDR                  P00670 camelus dro
    24    139    83.7    125  1  RNP_SPAEH                  P16414 spalax leuc
    25    139    83.7    128  1  RNP_CHOHO                  P00685 choloepus h
    26    139    83.7    148  1  RNP_GERNI                  Q9wus2 gerbillus n
    27    137    82.5    124  1  RNP_CHIBR                  P00675 chinchilla
    28    136    81.9    124  1  RNP_PIG                    P00671 sus scrofa
    29    136    81.9    141  1  RNBR_GIRCA                 Q29542 giraffa cam
    30    136    81.9    151  1  RNBR_AXIPR                 P87350 axis porcin
    31    136    81.9    152  1  RNP_RAT                    P00684 rattus norv
    32    135    81.3    128  1  RNP_MYOCO                  P00676 myocastor c
    33    135    81.3    148  1  RNP_MICNV                  Q9wuv3 microtus ni
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    34    135    81.3    151  1  RNBR_CAPCA                 P79351 capreolus c
    35    134    80.7    128  1  RNP_HYDHY                  P00677 hydrochoeru
    36    134    80.7    128  1  RNP_PROGU                  P04059 proechimys
    37    134    80.7    150  1  RNS_BOVIN                  P00669 bos taurus
    38    134    80.7    156  1  RNP_HUMAN                  P07998 homo sapien
    39    133    80.1    130  1  RNP_CRIGR                  P24717 cricetulus
    40    133    80.1    143  1  RNBR_SHEEP                 Q29543 ovis aries
    41    133    80.1    148  1  RNP_PERLE                  Q9wuv5 peromyscus
    42    133    80.1    149  1  RNP_MUSSA                  Q9qyx2 mus saxicol
    43    133    80.1    167  1  RNBR_BOVIN                 P39873 bos taurus
    44    131    78.9    148  1  RNP_CLEGL                  Q9wur4 clethrionom
    45    131    78.9    149  1  RNP_ACOCA                  Q9wut5 acomys cahi

                              ALIGNMENTS

RESULT 1
RNP_BOVIN
ID   RNP_BOVIN      STANDARD;      PRT;   150 AA.
AC   P00656;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   RIBONUCLEASE PANCREATIC PRECURSOR (EC 3.1.27.5) (RNASE 1) (RNASE A).
GN   RNASE1 OR RNS1.
OS   Bos taurus (Bovine), and Bison bison (American bison).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913, 9901;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Bovine;
RX   MEDLINE=88262557; PubMed=2456818;
RA   Carsana A., Confalone E., Palmieri M., Libonati M., Furia A.;
RT   "Structure of the bovine pancreatic ribonuclease gene: the unique
RT   intervening sequence in the 5' untranslated region contains a
RT   promoter-like element.";
RL   Nucleic Acids Res. 16:5491-5502(1988).
RN   [2]
RP   SEQUENCE OF 27-150 FROM N.A.
RC   SPECIES=Bovine;
RX   MEDLINE=96093920; PubMed=7479688;
RA   delCardayre S.B., Ribo M., Yokel E.M., Quirk D.J., Rutter W.J.,
RA   Raines R.T.;
RT   "Engineering ribonuclease A: production, purification and
RT   characterization of wild-type enzyme and mutants at Gln11.";
RL   Protein Eng. 8:261-273(1995).
RN   [3]
RP   SEQUENCE OF 27-150, AND DISULFIDE BONDS.
RC   SPECIES=Bovine;
RA   Smyth D.G., Stein W.H., Moore S.;
RT   "The sequence of amino acid residues in bovine pancreatic
RT   ribonuclease: revisions and confirmations.";
RL   J. Biol. Chem. 238:227-234(1963).
RN   [4]
RP   SEQUENCE OF 27-150.
RC   SPECIES=Bovine;
RA   Plummer T.H. Jr., Hirs C.H.W.;
RT   "On the structure of bovine pancreatic ribonuclease B. Isolation of
RT   a glycopeptide.";
RL   J. Biol. Chem. 239:2530-2538(1964).
RN   [5]
RP   ACTIVE SITE.
RC   SPECIES=Bovine;
RA   Heinrikson R.L., Stein W.H., Crestfield A.M., Moore S.;
RT   "The reactivities of the histidine residues at the active site of
RT   ribonuclease toward halo acids of different structures.";
RL   J. Biol. Chem. 240:2921-2934(1965).
RN   [6]
RP   ACTIVE SITE.
RC   SPECIES=Bovine;
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RX   MEDLINE 69260123; PubMed 5801478;
RA   Shall S., Barnard E.A.;
RT   "Heavy atom labelled derivatives of bovine pancreatic ribonuclease
RT   I. Specific reactions of ribonuclease with N acetylhomocysteine
RT   thiolactone and silver ion.";
RL   J. Mol. Biol. 41:237 251(1969).
RN   [7]
RP   X RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC   SPECIES Bovine;
RX   MEDLINE 70092235; PubMed 5460889;
RA   Wyckoff H.W., Tsernoglou D., Hanson A.W., Knox J.R., Lee B.,
RA   Richards F.M.;
RT   "The three dimensional structure of ribonuclease-S. Interpretation of
RT   an electron density map at a nominal resolution of 2 A.";
RL   J. Biol. Chem. 245:305 328(1970).
RN   [8]
RP   X RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RC   SPECIES Bovine;
RX   MEDLINE 74253324; PubMed 4835726;
     Carlisle C.H., Palmer R.A., Mazumdar S.K., Gorinsky B.A.,
     Yeates D.G.R.;
     "The structure of ribonuclease at 2.5 A resolution.";
     J. Mol. Biol. 85:1 18(1974).
RN   [9]
RP   X RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC   SPECIES Bovine;
RX   MEDLINE 82120062; PubMed 6276380;
RA   Wlodawer A., Bott R., Sjoelin L.;
RT   "The refined crystal structure of ribonuclease A at 2.0-A
RT   resolution.",
RL   J. Biol. Chem. 257:1325 1332(1982).
RN   [10]
RP   X RAY CRYSTALLOGRAPHY (1.26 ANGSTROMS).
RC   SPECIES Bovine;
RX   MEDLINE 88294009; PubMed-3401445;
RA   Wlodawer A., Svensson L.A., Sjoelin L., Gilliland G.L.;
RT   "Structure of phosphate-free ribonuclease A refined at 1.26 A.",
RL   Biochemistry 27:2705 2717(1988).
RN   [11]
RP   X RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX   MEDLINE 97299793; PubMed=9154942;
RA   Leonidas D.D., Shapiro R., Irons L.I., Russo N., Acharya K.R.;
RT   "Crystal structures of ribonuclease A complexes with 5'
RT   diphosphoadenosine 3' phosphate and 5' diphosphoadenosine
RT   2' phosphate at 1.7 A resolution.";
RL   Biochemistry 36:5578 5588(1997).
RN   [12]
RP   STRUCTURE BY NMR.
RC   SPECIES Bovine;
RX   MEDLINE 89375325; PubMed 2775743;
RA   Robertson A.D., Purisima E.O., Eastman M.A., Scheraga H.A.;
     "Proton NMR assignments and regular backbone structure of bovine
     pancreatic ribonuclease A in aqueous solution.";
     Biochemistry 28:5930 5938(1989).
     [13]
RP   STRUCTURE BY NMR.
RC   SPECIES Bovine;
RX   MEDLINE 89377830; PubMed 2776756;
RA   Rico M., Bruix M., Santoro J., Gonzalez C., Neira J.L., Nieto J.L.,
RA   Herranz J.;
RT   "Sequential 1H-NMR assignment and solution structure of bovine
RT   pancreatic ribonuclease A.";
RL   Eur. J. Biochem. 183:623 638(1989).
RN   [14]
RP   STRUCTURE BY NMR.
RC   SPECIES Bovine;
RX   MEDLINE 93044359; PubMed 1841699;
RA   Rico M., Santoro J., Gonzalez C., Bruix M., Neira J.L., Nieto J.L.,
RA   Herranz J.;
RT   "3D structure of bovine pancreatic ribonuclease A in aqueous
RT   solution: an approach to tertiary structure determination from a
RT   small basis of 1H NMR NOE correlations.";
RL   J. Biomol. NMR 1:283 298(1991).
RN   [15]
RP   DNA-BINDING.
RC   SPECIES Bovine;
RX   MEDLINE-86179900; PubMed-3961503;
RA   McPherson A., Brayer G., Cascio D., Williams R.;
RT   "The mechanism of binding of a polynucleotide chain to pancreatic
RT   ribonuclease.";
RL   Science 232:765-768(1986).
RN   [16]
RP   SEQUENCE OF 27-150.
RC   SPECIES B.bison;
RX   MEDLINE=76259396; PubMed 955781;
RA   Muskiet F.A.J., Welling G.W., Beintema J.J.;
RT   "Studies on the primary structure of bison pancreatic ribonuclease.";
RL   Int. J. Pept. Protein Res. 8:345-348(1976).
CC   -!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC       NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P
CC       WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC    !  TISSUE SPECIFICITY: PANCREAS.
CC   -!- MISCELLANEOUS: RIBONUCLEASE CAN DESTABILIZE OR UNWIND THE DNA
CC       HELIX BY COMPLEXING WITH SINGLE-STRANDED DNA; THIS COMPLEX ARISES
CC       BY AN EXTENDED MULTISITE CATION-ANION INTERACTION BETWEEN THE
CC       LYSINE AND ARGININE RESIDUES OF THE ENZYME AND THE PHOSPHATE
CC       GROUPS OF THE NUCLEOTIDES.
CC   -!- MISCELLANEOUS: THE BISON SEQUENCE APPEARS TO BE IDENTICAL WITH
CC       THAT OF BOVINE.
CC   -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC   -!- DATABASE: NAME Worthington enzyme manual;
CC       WWW="http://www.worthington-biochem.com/manual/R/RNASE.html".
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X07283; CAA30263.1; -.
DR   EMBL; S80747; AAB35594.1; -.
DR   PIR; A00804; NRBO.
DR   PIR; A91771; NRBOB.
DR   PIR; A32471; A32471.
DR   PIR; S00897; S00897.
DR   PIR; S05528; S05528.
DR   PDB; 1RBB; 15-JUL-92.
DR   PDB; 3RN3; 15-OCT-91.
DR   PDB; 2RNS; 31-JAN-94.
DR   PDB; 1RSM; 15-OCT-89.
DR   PDB; 1SRN; 15-JUL-92.
DR   PDB; 5RSA; 15-APR-93.
DR   PDB; 6RSA; 15-OCT-89.
DR   PDB; 7RSA; 15-JAN-93.
DR   PDB; 8RSA; 15-APR-91.
DR   PDB; 9RSA; 15-APR-91.
DR   PDB; 1RAT; 15-JUL-93.
DR   PDB; 2RAT; 15-JUL-93.
DR   PDB; 3RAT; 15-JUL-93.
DR   PDB; 4RAT; 15-JUL-93.
DR   PDB; 5RAT; 15-JUL-93.
DR   PDB; 6RAT; 15-JUL-93.
DR   PDB; 7RAT; 15-JUL-93.
DR   PDB; 8RAT; 15-JUL-93.
DR   PDB; 9RAT; 15-JUL-93.
DR   PDB; 1RBC; 31-OCT-93.
DR   PDB; 1RBD; 31-OCT-93.
DR   PDB; 1RBE; 31-OCT-93.
DR   PDB; 1RBF; 31-OCT-93.
DR   PDB; 1RBG; 31-OCT-93.
DR   PDB; 1RBH; 31-OCT-93.
DR   PDB; 1RBI; 31-OCT-93.
DR   PDB; 1RBJ; 07-DEC-95.
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  Query Match             100.0%;  Score 166;  DB 1;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-17;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0

Qy        1 CAYKTTQANKHIIVACEGNPYVPVHFDASV 30
            ||||||||||||||||||||||||||||||
Db      121 CAYKTTQANKHIIVACEGNPYVPVHFDASV 150


RESULT   2
RNP_BUBBU
ID   RNP_BUBBU      STANDARD;      PRT;   124 AA.
AC   P00657;
DT   21-JUL-1986 (Rel. 01, Created)
     13-AUG-1987 (Rel. 05, Last sequence update)
     20-AUG-2001 (Rel. 40, Last annotation update)
     RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).
GN   RNASE1 OR RNS1.
OS   Bubalus bubalis (Domestic water buffalo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bubalus.
OX   NCBI_TaxID=89462;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=SWAMP BREED, AND RIVER BREED;
RX   MEDLINE=80153329; PubMed=540006;
RA   Sidik A., Martena B., Beintema J.J.;
RT   "Amino acid sequence differences in pancreatic ribonucleases from
RT   water buffalo breeds from Indonesia and Italy.";
RL   Biochem. Genet. 17:1151-1158(1979).
RN   [2]
RP   SEQUENCE.
RC   STRAIN=SWAMP BREED, AND RIVER BREED;
RX   MEDLINE=80109825; PubMed=7353035;
RA   Beintema J.J.;
RT   "Primary structures of pancreatic ribonucleases from Bovidae. Impala,
RT   Thomson's gazelle, nilgai and water buffalo.";
RL   Biochim. Biophys. Acta 621:89-102(1980).
CC   -!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC       NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P
CC       WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- TISSUE SPECIFICITY: PANCREAS.
CC   -!- PTM: SWAMP BREED RIBONUCLEASE DO NOT BIND CARBOHYDRATE, BUT THERE
         IS EVIDENCE OF A POLYMORPHIC FORM THAT DOES.
     -!- MISCELLANEOUS: THE SEQUENCE OF THE RIVER BREED (ITALY) IS SHOWN,
         THE OTHER TYPE IS KNOWN AS SWAMP-TYPE (INDONESIA).
     -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR   PIR; A00805; NRWB.
DR   PIR; S08548; S08548.
DR   PIR; S08549; S08549.
DR   HSSP; P00656; 1SSB.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     34     34       N-LINKED (GLCNAC...) (IN RIVER-BREED
FT                                ONLY).
FT   VARIANT      34     34       N -> S (IN SWAMP BREED).
FT   VARIANT      61     61       E -> K (IN SWAMP BREED).
FT   VARIANT     120    120       Y -> F (IN SWAMP BREED).
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SQ   SEQUENCE   124 AA;  13[illegible] MW;  [illegible] CRC64;

  Query Match             9[illegible].2%;  Score 16[illegible];  DB [illegible];  Length 124;
  Best Local Similarity   96.7%;  Pred. No. [illegible];
  Matches   29;  Conservative    1;  Mismatches    [illegible];  Indels    0;  Gaps    0;

Qy        1 CAYKTTQANKHIIVACEGNPYVPVHFDASV 30
            ||||||||||||||||||||||||||:|||
Db       95 CAYKTTQANKHIIVACEGNPYVPVHYDASV 124


RESULT   3
RNP_AEPME
ID   RNP_AEPME      STANDARD;      PRT;   124 AA.
AC   P07847;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).
GN   RNASE1 OR RNS1.
OS   Aepyceros melampus (Impala).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea.
OC   Bovidae; Aepycerotinae; Aepyceros.
OX   NCBI_TaxID=9897;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=80109825; PubMed=7353035;
RA   Beintema J.J.;
RT   "Primary structures of pancreatic ribonucleases from Bovidae. Impala,
RT   Thomson's gazelle, nilgai and water buffalo.";
RL   Biochim. Biophys. Acta 621:89-102(1980).
CC   -!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC       NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P
CC       WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- TISSUE SPECIFICITY: PANCREAS.
CC   -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR   PIR; S07141; S07141.
DR   HSSP; P00656; 1SSC.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   CARBOHYD     34     34       N-LINKED (GLCNAC...) (PARTIAL).
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
SQ   SEQUENCE   124 AA;  13[illegible] MW;  [illegible] CRC64;


  Query Match             9[illegible].4%;  Score 1[illegible];  DB [illegible];  Length 124;
  Best Local Similarity   96.7%;  Pred. No. [illegible];
  Matches   29;  Conservative    [illegible];  Mismatches    1;  Indels    [illegible];  Gaps    0;

Qy        1 CAYKTTQANKHIIVACEGNPYVPVHFDASV 30
            |||||||| |||||||||||||||||||||
Db       95 CAYKTTQAKKHIIVACEGNPYVPVHFDASV 124


RESULT   4
RNP_GAZTH
ID   RNP_GAZTH      STANDARD;      PRT;   124 AA.
AC   P07848;
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DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).
GN   RNASE1 OR RNS1.
OS   Gazella thomsonii (Thomson's gazelle).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Antilopinae; Gazella.
OX   NCBI_TaxID=69308;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80189825; PubMed=7353035;
RA   Beintema J.J.;
RT   "Primary structures of pancreatic ribonucleases from Bovidae. Impala,
RT   Thomson's gazelle, nilgai and water buffalo.";
RL   Biochim. Biophys. Acta 621:89-103(1980).
CC   -!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC       NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P
         WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
     -!- SUBCELLULAR LOCATION: SECRETED.
     -!- TISSUE SPECIFICITY: PANCREAS.
     -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR   PIR; S08546; S08546.
DR   HSSP; P00656; 1SSC.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     34     34       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   124 AA;  13763 MW;  23DE46BA811D20C6 CRC64;

  Query Match             96.4%;  Score 160;  DB 1;  Length 124;
  Best Local Similarity   96.7%;  Pred. No. 8.8e-17;
  Matches   29;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CAYKTTQANKHIIVACEGNPYVPVHFDASV 30
              |||||||| |||||||||||||||||||||
Db         95 CAYKTTQAQKHIIVACEGNPYVPVHFDASV 124


  ULT   5
  SHEEP
     RNP_SHEEP      STANDARD;      PRT;   124 AA.
AC   P00661; P04429;
DT   21-JUL-1986 (Rel. 01, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).
GN   RNASE1 OR RNS1.
OS   Ovis aries (Sheep), and Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940, 9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Sheep, and C.hircus;
RX   MEDLINE=96139017; PubMed=8587129;
RA   Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA   Vento M.T., Furia A.;
RT   "Molecular evolution of genes encoding ribonucleases in ruminant
```

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RT   species.";
RL   J. Mol. Evol. 41:850-858(1995).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=Sheep, and C.hircus; TISSUE=Pancreas;
RX   MEDLINE=74309062; PubMed=4855110;
RA   Welling G.W., Scheffer A.J., Beintema J.J.;
RT   "The primary structure of goat and sheep pancreatic ribonucleases.";
RL   FEBS Lett. 41:58-61(1974).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=Sheep;
RX   MEDLINE=74025520; PubMed=4356260;
RA   Kobayashi R., Hirs C.H.W.;
RT   "The amino acid sequence of ovine pancreatic ribonuclease A.";
RL   J. Biol. Chem. 248:7833-7837(1973).
CC   -!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC       NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P
CC       WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- TISSUE SPECIFICITY: PANCREAS.
CC   -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; S81741; AAB36135.1; -.
DR   EMBL; S81742; AAB36136.1; -.
DR   PIR; A00809; NRSH.
DR   PIR; A00810; NRGT.
DR   HSSP; P00656; 1SSC.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84
FT   DISULFID     40     95
FT   DISULFID     58    110
FT   DISULFID     65     72
FT   ACT_SITE     12     12
FT   ACT_SITE     41     41
FT   ACT_SITE    119    119
FT   CARBOHYD     34     34       N-LINKED (GLCNAC. . .) (PARTIAL).
FT   CONFLICT     49     49       E -> Q (IN REF. 3).
FT   CONFLICT    103    103       E -> Q (IN REF. 3).
SQ   SEQUENCE   124 AA;  13707 MW;  3570EC14528EDDFA CRC64;

  Query Match             96.4%;  Score 160;  DB 1;  Length 124;
  Best Local Similarity   96.7%;  Pred. No. 8.8e-17;
  Matches   29;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CAYKTTQANKHIIVACEGNPYVPVHFDASV 30
              |||||||| |||||||||||||||||||||
Db         95 CAYKTTQAKKHIIVACEGNPYVPVHFDASV 124


RESULT   6
RNP_ANTAM
ID   RNP_ANTAM      STANDARD;      PRT;   124 AA.
AC   P00668;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).
```

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GN   RNASE1 OR RNS1.
OS   Antilocapra americana (Pronghorn).
OC   Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi,
OC   Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
OC   Antilocapridae; Antilocapra.
OX   NCBI_TaxID-9891;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE 80075014; PubMed-513141;
RA   Beintema J.J., Gaastra W., Munniksma J.;
RT   "Primary structure of pronghorn pancreatic ribonuclease: close
RT   relationship between giraffe and pronghorn.";
RL   J. Mol. Evol. 13:305-316(1979).
CC   -!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC       NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P
CC       WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- TISSUE SPECIFICITY: PANCREAS.
CC   -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR   PIR; A00813; NRPRH.
DR   HSSP; P00656; 1RBC.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     34     34       N-LINKED (GLCNAC. . .) (PARTIAL).
SQ   SEQUENCE   124 AA;  13711 MW;  9435EF532420F852 CRC64;


  Query Match             94.6%,  Score 157,  DB 1,  Length 124,
  Best Local Similarity   93.3%;  Pred. No. 2.4e-16;
  Matches   28;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0,

Qy          1 CAYKTTQANKHIIVACEGNPYVPVHFDASV 30
              |||||||| ||||:| .||||||||:||||
Db         95 CAYKTTQAKKHIIVACEGNPYVPVHYDASV 124


RESULT   7
RNP_ALCAA
ID   RNP_ALCAA      STANDARD;      PRT;   124 AA.
AC   P00667;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).
GN   RNASE1 OR RNS1.
OS   Alces alces alces (European moose) (Elk).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Alces.
OX   NCBI_TaxID-985[illegible].
RN   [1]
RP   PARTIAL SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE-76003215; PubMed 1157925.
RA   Leijenaar-Van den Berg G., Beintema J.J.;
RT   "The amino acid sequences of reindeer, moose and fallow deer
RT   pancreatic ribonucleases.";
RL   FEBS Lett. 56:101-107(1975).
CC   -!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC       NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P
```

```
CC       WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- TISSUE SPECIFICITY: PANCREAS.
CC   -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR   PIR; C91418; NREKN.
DR   HSSP; P00656; 1SSC.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     34     34       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   124 AA;  1[illegible] MW;  [illegible] CRC64;


  Query Match             [illegible]4.[illegible]%,  Score 1[illegible],  DB [illegible],  Length 124;
  Best Local Similarity   [illegible]3.3%;  Pred. No. [illegible];
  Matches   28;  Conservative    [illegible];  Mismatches    2;  Indels    [illegible];  Gaps    0;

Qy          1 CAYKTTQANKHIIVACEGNPYVPVHFDASV [illegible]
              | .| ||| ||| |.||||.:|    .||
Db         95 CVYKTTQAEKHIIVACEGNPYVPVHFDASV 124


RESULT   8
RNP_CAPCA
ID   RNP_CAPCA      STANDARD;      PRT;   124 AA.
AC   P00664;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).
GN   RNASE1 OR RNS1.
OS   Capreolus capreolus (Roe deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Capreolus.
OX   NCBI_TaxID=9858;
RN   [1]
RP   SEQUENCE
RC   TISSUE=Pancreas;
RX   MEDLINE=73253236; PubMed 47[illegible]302;
RA   Zwiers H., Scheffer A.J., Beintema J.J.;
RT   "Amino-acid sequences of red deer and roe deer pancreatic
RT   ribonucleases.";
RL   Eur. J. Biochem. 36:569-574(1973)
RN   [2]
RP   REVISIONS.
RX   MEDLINE 77112628; PubMed [illegible];
RA   Oosterhuis S., Welling G.W., Gaastra W., Beintema J.J.;
RT   "Reinvestigation of the primary structures of red deer and roe deer
RT   pancreatic ribonuclease and [illegible] mammalian
RT   ribonucleases.";
RL   Biochim. Biophys. Acta 4[illegible]
RN   [3]
RP   SEQUENCE FROM N.A
RX   MEDLINE 98278842; PubMed 9611269;
RA   Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
RA   Beintema J.J.;
RT   "Secretory ribonuclease genes and pseudogenes in true ruminants."
RL   Gene 212:259-268(1998).
CC   -!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC       NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P
CC       WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
```

```
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- TISSUE SPECIFICITY: PANCREAS.
CC   -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Y11672; CAA72377.1; -.
DR   PIR; A00613; NRDE.
DR   HSSP; P00656; 1SSC.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     34     34       N-LINKED (GLCNAC. . .) (PARTIAL).
SQ   SEQUENCE   124 AA;  13813 MW;  3836B2017625C613 CRC64;

  Query Match             94.0%;  Score 156;  DB 1;  Length 124;
  Best Local Similarity   93.3%;  Pred. No. 3.4e-16;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CAYKTTQANKHIIVACEGNPYVPVHFDASV 30
              | |||||| |||||||||||||||||||||
Db         95 CVYKTTQAEKHIIVACEGNPYVPVHFDASV 124


RESULT 9
RNP_RANIA
ID   RNP_RANIA      STANDARD;      PRT;   124 AA.
AC   P00666;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).
GN   RNASE1 OR RNS1.
OS   Rangifer tarandus (Reindeer) (Caribou).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Rangifer.
OX   NCBI_TaxID=9870;
RN   [1]
RP   PARTIAL SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=76003215; PubMed=1157925;
RA   Leijenaar-Van den Berg G., Beintema J.J.;
RT   "The amino acid sequences of reindeer, moose and fallow deer
RT   pancreatic ribonucleases.";
RL   FEBS Lett. 56:101-107(1975).
CC   -!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC       NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P
CC       WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- TISSUE SPECIFICITY: PANCREAS.
CC   -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR   PIR; B01418; NRDEN.
DR   HSSP; P00656; 1SSC.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
SQ   SEQUENCE   124 AA;  13759 MW;  CE56B8BB9A87CD54 CRC64;

  Query Match             94.0%;  Score 156;  DB 1;  Length 124;
  Best Local Similarity   93.3%;  Pred. No. 3.4e-16;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CAYKTTQANKHIIVACEGNPYVPVHFDASV 30
              | |||||| |||||||||||||||||||||
Db         95 CVYKTTQAEKHIIVACEGNPYVPVHFDASV 124


RESULT 10
RNP_CONTA
ID   RNP_CONTA      STANDARD;      PRT;   124 AA.
AC   P00660;
DT   21-JUL-1986 (Rel. 01, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).
GN   RNASE1 OR RNS1.
OS   Connochaetes taurinus (Brindled gnu).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Alcelaphinae; Connochaetes.
OX   NCBI_TaxID=9927;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=76210818; PubMed=1278669;
RA   Groen G., Welling G.W., Beintema J.J.;
RT   "The amino acid sequence of gnu pancreatic ribonuclease.";
RL   FEBS Lett. 60:300-304(1975).
CC   -!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC       NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P
CC       WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- TISSUE SPECIFICITY: PANCREAS.
CC   -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR   PIR; A00808; NRGN.
DR   HSSP; P00656; 1SSC.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease.
FT   DISULFID     26     84
FT   DISULFID     40     95
FT   DISULFID     58    110
FT   DISULFID     65     72
FT   ACT_SITE     12     12
FT   ACT_SITE     41     41
FT   ACT_SITE    119    119
SQ   SEQUENCE   124 AA;  13686 MW;  3564BE9D9D871195 CRC64;

  Query Match             93.4%;  Score 155;  DB 1;  Length 124;
  Best Local Similarity   93.3%;  Pred. No. 4.8e-16;
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  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CAYKTIQANK-IIVACEGNPYVPVHFDASV 30
              | |: ||| |||  |||||||||||||||
Db         95 CAYKAIQAKK-IIVACEGNPYVPVHFDASV 124


Search completed: March 14, 2002, 17:35:02
Job time: 653 sec
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